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INFORMATION DISCLOSURE STATEMENT BY APPLICANT

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Sheet 1 of 4

Complete if Known	
Application Number	09/812,034
Filing Date	March 19, 2001
First Named Inventor	MAYO, Stephen L.
Group Art Unit	1631
Examiner Name	
Attorney Docket Number	A-65353-6/RFT/RMS/RMC

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	A1	Brenner and Berry, A., et al., "A quantitative methodology for the de novo design of proteins", Protein Sci. 3:1871-1882 (Oct. 1994).	
	A2	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) Oct. 6, 1997, 9-10 (1997).	
	A3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol.247:1306-1310 (Mar. 1990).	
	A4	Bowie, J.U., et al., "A Method to Identify Protein Sequences that Fold into a Known Three-Dimensional Structure", Science vol.253:164-170 (Jul. 1991).	
	A5	Brooks et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations," J. of Computational Chemistry, 4(2):187-217 (1983).	
	A6	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug. 1983).	
	A7	Cornell et al., "A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules," J. Am. Chem. Soc., 117:5179-5197 (1995).	
	A8	Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", Protein Science 6:1333-1337 (Jun. 1997).	
	A9	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).	
	A10	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).	
	A11	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol. 4, Suppl. 2, 83 (1995).	
	A12	Dahiyat et al., "Protein design Automation," Poster Sessions, Protein Science vol.5, Suppl. 1, 22-23 (1996).	
	A13	Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 278:82-87 (1997).	
	A14	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).	
	A15	Dahiyat et al., "Protein Design Automation," 1996, Protein Science, vol. 5, pp. 895-903, Nov. 30, 1999.	
	A16	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).	
	A17	Dalal, S., et al., "Protein alchemy: Changing .beta.-sheet into .alpha.-helix", Nature Struc. Biol. vol.4(7):548-552 (Jul. 1997).	

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	B2	Desjarlais, J.R., et al., "De novo design of the hydrophobic cores of proteins", Protein Science 4:2006-2018 (1995).	
	B3	Desjarlais et al., "New strategies in protein design," Current Opinion in Biotechnology :460-466 (1995).	
	B4	Desmet, J., et al., "The 'Dead End Elimination' Theorem: A New Approach to the Side Chain Packing Protein", from "The Protein Folding Problem and Tertiary Structure Prediction" Ch.10:1-49 (1994).	
	B5	Desmet, J., et al., "The dead-end elimination theorem and its use in protein side-chain positioning", Nature vol.356:539-542 (Apr. 1992).	
	B6	Desmet et al., "Theoretical and Algorithmical Optimization of the Dead-End Elimination Theorem," Proceedings of the Pacific Symposium on Biocomputing '97, 122-133 (1997).	
	B7	Dunbrack Jr., R.L., et al., "Conformational analysis of the backbone-dependent rotamer preferences of protein sidechains", Struc. Biol. vol.1(5):334-340 (May 1994).	
	B8	Eisenberg, D., et al., "Solvation energy in protein folding and binding", Nature vol.319:199-203 (Jan. 1986).	
	B9	Goldstein, R.F., "Efficient Rotamer Elimination Applied to Protein Side-Chains and Related Spin Glasses", Biophys. Jour. vol.66:1335-1340 (May 1994).	
	B10	Gordon et al. "Energy functions for protein design," Curr. Opinion in Struct. Biol., 9:509-513 (1999).	
	B11	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils," Proc. Natl. Acad. Sci. USA, 92:8408-8412 (1995).	
	B12	Harbury et al., "High-Resolution Protein Design with Backbone Freedom," Science, 282:1462-1467 (1998).	
	B13	Hellinga, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol. 222:763-785 (1991).	
	B14	Hellinga, H.W., "Rational protein design: Combining theory and experiment", Proc. Natl. Acad. Sci, USA vol.94:10015-10017 (Sep. 1997).	
	B15	Hellinga, H.W., et al., "Optimal sequence selection in proteins of known structure by simulated evolution", Proc. Natl. Acad. Sci., USA vol.91:5803-5807 (Jun. 1994).	
	B16	Holmes, "First-ever designer protein fits like a glove," New Scientist, IPC Magazines Limited, Oct. 11, 1997 (1997).	
	B17	Hurley et al., "Design and Structural Analysis of Alternative Hydrophobic Core Packing Arrangements in Bacteriophage T4 Lysozyme," J. Mol. Biol., 224:1143-1159(1992).	

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	C2	Koehl et al., "De Novo Protein Design. I. In Search of Stability and Specificity," J. Mol. Biol., 293:1161-1181 (1999).	
	C3	Kono et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction from Given Backbone Geometry," Proteins: Structure, Function, and Genetics, 19:244-255 (1994).	
	C4	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded β-Sheet Protein," Science, 281:253-256 (1988).	
	C5	Lasters et al., "Enhanced dead-end elimination in the search for the global minimum energy conformation of a collection of protein side chains," 1995, Protein Engineering, vol. 8, No. 8, pp. 815-822.	
	C6	Lasters, I., et al., "Dead-End Based Modeling Tools to Explore the Sequence Space That is Compatible with a Given Scaffold", Jour. of Protein Chem. vol.16(5):449-452 (Jul. 1997).	
	C7	Lazar et al., "De novo design of the hydrophobic core of ubiquitin," Protein Science 6:1167-1178 (1997).	
	C8	Lee et al., "Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core," Nature, 352:448-451 (1991).	
	C9	Lim et al., "The crystal structure of a mutant protein with altered but improved hydrophobic core packing," Proc Natl Acad Sci U S A. 1994 Jan 4;91(1):423-7	
	C10	Mayo et al., "DREIDING: A Generic Force Field for Molecular Simulations," J. Phys. Chem., 94:8897-8909 (1990).	
	C11	Minor Jr., D.L., "Measurement of the .beta.-sheet-forming propensities of amino acids", Nature vol.367:660-663 (Feb. 1994).	
	C12	Munoz, V., et al., "Helix design, prediction and stability", Curr. Opin. in Biotech. 6:382-386 (Aug. 1995).	
	C12	Munoz, V., et al., "Intrinsic Secondary Structure Propensities of the Amino Acids, Using Statistical phi-psi Matrices: Comparison with Experimental Scales", Proteins 20:301-311 (1994).	
	C14	Munoz, V., et al., "Analysis of the effect of local interactions on protein stability", Folding & Design 1(3):167-178 (Apr. 1996).	
	C15	Pabo, C., "Designing proteins and peptides", Nature vol.301:200 (Jan. 1983).	
	C16	Padmanabhan, S., et al., "Relative helix-forming tendencies of nonpolar amino acids", Nature vol.344:268-270 (Mar. 1990).	
	C17	Ponder, J.W., et al., "Use of Packing Criteria in the Enumeration of Allowed Sequences for Different Structural Classes", release by Acad. Press Inc. (London) Ltd. pp.775-791(1987).	
✓	C18	Rappe et al., "Charge Equilibration for Molecular Dynamics Simulations," J. Phys. Chem., 95:3358-3363 (1991).	

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	D2	Smith, C.K., et al., "Guidelines for Protein Design: The Energetics of .beta. Sheet Side Chain Interactions", Science vol.270:980-982 (Nov. 1995).	
	D3	Stickle et al., "Hydrogen Bonding in Globular Proteins," (1992) Journal of Molecular Biology, vol.226, pp. 1143-1159.	
	D4	Sun, S., et al., "Designing amino acid sequences to fold with good hydrophobic cores", Protein Eng. vol.8(12):1205-1213 (1995).	
	D5	Tuffery et al., "A New Approach to the Rapid Determination of Protein Side Chain Conformations," J. of Biomolecular Struct. & Dynamics, 8(6):1267-1289 (1991).	
	D6	van Gunsteren et al., "Prediction of the Activity and Stability Effects of Site-directed Mutagenesis on a Protein Core," J. Mol. Biol., 227:389-395 (1992).	
	D7	Villegas et al., "Stabilization of proteins by rational design of .alpha.-helix stability using helix/coil transition theory," Folding & Design, 1(1):29-34 (1995).	
	D8	Wesson et al., "Atomic solvation parameters applied to molecular dynamics of proteins in solution," Protein Science, 1:227-235 (1992).	
✓	D9	Wodak, S.J., et al., "Analytical approximation to the accessible surface area of proteins", Proc. Natl. Acad. Sci. USA vol.77(4):1736-1740 (Apr. 1980).	

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